+--+

FIGURE 1

when either binding to itself, to a synthetic ligand such as Rupe312, or binding to another hepreceptor. Note how the highly charged region matches positive to negative charges Primary/secondary structure of the Hepreceptor

Figure 1a: Inactive FOLDED conformation of the Hepreceptor

~ = continuity of aminoacid sequence p = phosphate group on tyrosine

Hinge	
domain A REEKHOKOLEROOLETEKK RRETVEREKEOM A H	LARQIQESLEREAKKTE TOOLRIMEEKERM OLARQIQESLEREAKTE TOOLRIMEEKERSENENE DISTRIBEREEKE TOOLKE TOOLKE TOOLKE TOOLKE
Hepreceptor1 Seq number Aminoacid Side chain charge	Side chain charge aminoacid seq number

Figure 1b: Active OPEN conformation of the Hepreceptor binding a ligand (Rupe312) KK-RRETVERE

Rupe312

Hepreceptor1 Inverted sequence Side chain charge aminoacid seq number	Hepreceptor1 Inverted sequence The control of the c	E E R A 308
rice to Dim	marisation between two Hepreceptors in the active	373
Ligare 1c. p.	4	6 X 2 X 3 X 3 X 3 X 3

AREEKHOKOLEROOLETEKK-RRETVEREKEOMMREKEELMLRLODYEEKTKKAERELSEOIGRALO Hepreceptor2 Sed number

-++ ++- - --+- +--+

Side chain charge

Aminoacid

OLARO I GESLEREAKK TKEEY DOLRLM LEEKERMMOEKEREV TERR - KKETEL GOREL OKOHKEERA 373 Side chain charge sed number aminoacid

domain B

inverted sequence Hepreceptor1

PCT/GB00/03566

' WO 01/25275 FIGURE 2

Cellular locations and complexes of ezrin

